

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	DB			
C 1	404.4	30.5	658	14	BO135057	INIT1_2_G	BO135057 INIT1_2_G
C 2	389.4	29.4	607	14	BO134912	INIT1_1_F	BO134912 INIT1_1_F
C 3	367.6	27.9	602	14	BO135164	INIT1_4_B	BO135164 INIT1_4_B
C 4	366.6	27.6	590	14	BO135179	INIT1_4_C	BO135179 INIT1_4_C
C 5	317.1	23.9	501	14	BO134889	INIT1_1_D	BO134889 INIT1_1_D
C 6	316.6	23.9	675	14	BO135186	INIT1_1_E	BO135186 INIT1_1_E

VERSION	BQ134912.1	EST	High quality sequence stop: 658
KEYWORDS	EST.	LOCUS	POLYA=No. Location/Qualifiers
SOURCE	1. 658	ORGANISM	/organism="Ichthyophthirius multifiliis"
FEATURES	/strain="G5"	REFERENCE	/db_xref="taxon:5932"
source		AUTHORS	/clone_lib="G5 trophont cDNA (INIT1)"
		JOURNAL	/note="Vector: pBluescript SK(-) from Lambda Zap II;"
		COMMENT	Site_1: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain.
			Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into Lambda ZAP II. Plasmid DNA for sequencing was prepared by mass sequencing."
BASE COUNT	215 a 122 c 122 g 199 t	FEATURES SOURCE	Score 404.4; DB 14; Length 658; Best Local Similarity 77.1%; Pred. No. 1.3e-76; Matches 49; Conservative 0; Mismatches 146; Indels 0; Gaps 0;
ORIGIN		QY 689 CTTAAAGTGAAAGCTCCCTGGCTTAAGCTTGTGCTGGCTCGCTGAGGTGTTG 748	QY 689 CTTAAAGTGAAAGCTCCCTGGCTTAAGCTTGTGCTGGCTCGCTGAGGTGTTG 748
		Db 653 CTCAGGGTAATGTGCAAATCTGTATGCGTGTACTGCTGCTGGCACTGT 808	Db 653 CTCAGGGTAATGTGCAAATCTGTATGCGTGTACTGCTGCTGGCACTGT 808
		QY 749 CTGGCTTAAGCTAGTTAATGTGCACTTGTGCTGGCTCGCTGAGGTGTTG 534	QY 749 CTGGCTTAAGCTAGTTAATGTGCACTTGTGCTGGCTCGCTGAGGTGTTG 534
		Db 593 CTGGCCCTTAATGCTGAAATGCTGAGCTGCAATCCTAATCCAGAT 868	Db 593 CTGGCCCTTAATGCTGAAATGCTGAGCTGCAATCCTAATCCAGAT 868
		QY 809 CAGGTGCTTAAGCTTAATTGCCCCACATAATGCGACTTGTGCAACTGCAA 474	QY 809 CAGGTGCTTAAGCTTAATTGCCCCACATAATGCGACTTGTGCAACTGCAA 474
		Db 533 CAGGTGCTGAGCTTAATTGCCCCACATAATGCGCACTGTGCACTCTTG 928	Db 533 CAGGTGCTGAGCTTAATTGCCCCACATAATGCGCACTGTGCACTCTTG 928
		QY 869 TTCAAGACGGAGTGCACUTGTTTTAGTAATTCTCACATAATGTTCAATGCAATTG 414	QY 869 TTCAAGACGGAGTGCACUTGTTTTAGTAATTCTCACATAATGTTCAATTG 414
		Db 473 TTACGACGGAGTAACCTACTATGATCACTCTCAATAATGTTCAATTGTAATTGTAAGG 988	Db 473 TTACGACGGAGTAACCTACTATGATCACTCTCAATAATGTTCAATTGTAATTGTAAGG 988
		QY 929 CTAATTACTTTTTAATGGTAATTGCAAGCAGTAAAGTTAATGTTAAGTGTCCAG 354	QY 929 CTAATTACTTTTTAATGGTAATTGCAAGCAGTAAAGTTAATGTTAAGTGTCCAG 354
		Db 413 CTGGCTTTTAAATGAAATGAAATGAAATGAAATGAAATGAAATGTTGTCAG 354	Db 413 CTGGCTTTTAAATGAAATGAAATGAAATGAAATGAAATGAAATGTTGTCAG 354
		QY 989 TAAGCTAAACTACCTCCAGAACATGCTCCAGTAATGCTACTTAAATGTT 1048	QY 989 TAAGCTAAACTACCTCCAGAACATGCTCCAGTAATGCTACTTAAATGTT 1048
		Db 353 TAAGCTAAACTACCTCCAGAACATGCTCCAGTAATGCTACTTAAATGTT 294	Db 353 TAAGCTAAACTACCTCCAGAACATGCTCCAGTAATGCTACTTAAATGTT 294
		QY 1049 TGACCACTATGCTGGTGTGAGTGTGAACTCAACTTAATTTGTAAGCTT 1108	QY 1049 TGACCACTATGCTGGTGTGAGTGTGAACTCAACTTAATTTGTAAGCTT 1108
		Db 293 AAAACGATTGCCCTCTGGTACAGTGGTATGTTGTCAGTAACTTGTGCTT 234	Db 293 AAAACGATTGCCCTCTGGTACAGTGGTATGTTGTCAGTAACTTGTGCTT 234
		QY 1109 CGCAACTGAATGACTAAATGTTCTGCTGCTTGTGAACTGCTTTTA 1168	QY 1109 CGCAACTGAATGACTAAATGTTCTGCTGCTTGTGAACTGCTTTTA 1168
		Db 233 TAGCAAGTGAATGACTAAATGTTAGCTTAATGCAATAAACATCTGGTTG 174	Db 233 TAGCAAGTGAATGACTAAATGTTAGCTTAATGCAATAAACATCTGGTTG 174
		QY 1169 CAGCAGTGTGAACTGATGACTGATGACTAAATTAATCTCTGTCACACTA 1228	QY 1169 CAGCAGTGTGAACTGATGACTGATGACTAAATTAATCTCTGTCACACTA 1228
		Db 173 CAGCAGTGTGAACTGATGACTAAATGTTAGCTTAATCTCTGGCTACACTA 114	Db 173 CAGCAGTGTGAACTGATGACTAAATGTTAGCTTAATCTCTGGCTACACTA 114
		QY 1229 AAGTATAGTGTGAACTGATGACTAAAGTAAATGCTGCCACACTACTTGCTAAATT 1288	QY 1229 AAGTATAGTGTGAACTGATGACTAAAGTAAATGCTGCCACACTACTTGCTAAATT 1288
		Db 113 AAGTATAGTGTGAACTGATGACTAAAGTAAATGCTGCCACACTACTTGCTAAATT 54	Db 113 AAGTATAGTGTGAACTGATGACTAAAGTAAATGCTGCCACACTACTTGCTAAATT 54
		QY 1289 TATCGATTTCCTTATTATTATTCTCTTATTATTG 1326	QY 1289 TATCGATTTCCTTATTATTATTCTCTTATTATTG 1326
		Db 53 TATCAATGTCCTTAATATTATTCTCTTATTATTG 16	Db 53 TATCAATGTCCTTAATATTATTCTCTTATTATTG 16



Query Match										source
Best Local Similarity 27.6%	Score 366.6;	DB 14;	Length 590;							1. .502 /organism="Ichthyophthirius multifiliis" /strain="G5" /db_xref="Taxon:5932"
Matches 423; Conservative 0; Mismatches 94; Indels 0; Gaps 0;										/clone.lib="G5 tropheont CDNA (INIT1)" /note="Vector: Bluescript SK(-) from Lambda Zap II; Site_1: EcoRI; Site_2: EcoRI; The library was made from tropheont polyA+ RNA of the G5 parasite strain. Double stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into Lambda Zap II. Plasmid DNA for sequencing was prepared by mass excision."
										II. Plasmid DNA for sequencing was prepared by mass excision."
Qy 810 AGGTGCCTAAGCTTAATGACAGATAATGCACTTAATGCTCCAACTGCAAT 869										BASE COUNT 185 a
Db 590 AGGTCTGAGCTTAATGAGCTAAATGAGCTAAATGTCGACTGAATGCTGGACTCTGT 531										80 c
Qy 870 TCAAGCGGAGTGACACTGTGTTAGTAATCATCCACATATAATGATCATG 929										70 g
Db 530 TACAGGGAGTAACCTACTATACATCTCATATGCTTAATGTAAAGC 471										167 t
Qy 930 TAATTACTTTTAATGTTAATGGTAAAGTTAAAGTTAATGTTAACGTGCCCAGT 989										
Db 470 TGGCTTTTACTAAATGTTAATGGTAAAGCTGAACTGATAATGTTGAGT 411										
Qy 990 AGTAAACACTGCTGCGTGGTACAGTACTGCTCGAGTAATACTGCTACTTAATGCCACATAATGTT 1049										
Db 410 AGTAAACACTGGTCAGCACTGCTGCGTAAATGCTGACTCATCAATAATTTA 351										
Qy 1050 GACCACATGTCCTGCGTGGTACAGTACTGCTCGAGTAATACTGCTACTTAATGCCACATAATGTT 1109										
Db 350 AACGATTGCGCTGCGTGGTACAGTGTGTTGATGAGNGTACATAACTAATTGTTAGCTTT 291										
Qy 1110 CGCAACTGAAATGACTAAATGTTGCTGTTTGTGATCAAAAAACTGGTTAAC 1169										
Db 290 AGGAGTGAAGTGACTAAATGTTAGCTAAATGCTGATCAAAATCTGGTTG 231										
Qy 1170 ACCAGGACTGATACATGTTGACTGAAATGTTAAACTCTGCGCACAGCTAA 1229										
Db 230 AGGAGGACTGATACATGTTGACTGAAATGTTGCTTAAAGATACTCTGTGCTACAGCTAA 171										
Qy 1230 AGTATANGCTGAGGTACTCAAAGTATAATGGCCCTCCAACTTCTGCTAAATTTT 1289										
Db 170 AGTATANGCTGAGGTACTTAAAGCTATAATGGCCCACTTTCGCAAAATTTT 111										
Qy 1290 ATCGATTCCATTATTATTTCTCTTCTATTATGTTG 1326										
Db 110 ATCAAATGTCCTTAAATTTATTCCTTCTATTATGTTG 74										
RESULT 5										
LOCUS BQ134889/c	502 bp	mRNA	linear	EST	22-APR-2002					RESULT 6
DEFINITION INIT1_1-D07_b1 A006 G5 tropheont CDNA (INIT1) Ichthyophthirius										LOCUS BQ13519/c
ORGANISM Ichthyophthirius multifiliis										DEFINITION INIT1_4-E06.g1-A006 G5 tropheont CDNA (INIT1) Ichthyophthirius
DEFINITION 1 (bases 1 to 502)										ORGANISM multifiliis mRNA sequence.
REFERENCE Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,										REFERENCE 1 (bases 1 to 675)
AUTHORS Dickerson,H., Lin,T.-L. and Pratt,L.H.										AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
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JOURNAL Laboratory for Genomics and Bioinformatics										JOURNAL Laboratory for Genomics and Bioinformatics
COMMENT The University of Georgia, Department of Plant Biology										COMMENT The University of Georgia, Department of Plant Biology
ORGANISM Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA										ORGANISM Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
SOURCE Hymenostomatida; Ophryogenina; Ichthyophthirius										SOURCE Hymenostomatida; Ophryogenina; Ichthyophthirius.
REFERENCE 1 (bases 1 to 502)										REFERENCE 1 (bases 1 to 675)
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COMMENT										



Qy 1146 TGGATCAAACAAACTGGTTACAGGGTACTGATCACAGTGAATGACTAAAAA 1205  
 Db 204 TGATCAAACAAATCTGGTTGAGGGTACTGATCACAGTGAATGACTAAAAA 145

Qy 1206 ATAACTCTGGTGCACAGCTAAAGTATGCTGAAGCTACTCAAACATAATGCGC 1265  
 Db 144 ATAACTCTGGTGCACAGCTAAAGTATGCTGAAGCTACTCAAACATAATGCGC 85

Qy 1266 CTCACTPACTTGCTAAATTGATGATGCTTATGATGCTTATGATGCTTATGCTTATT 1322  
 Db 84 CAGTCCACTTCGCAAAATTGATGCTTATGATGCTTATGATGCTTATT 28

RESULT 8  
 LOCUS BQ135036 419 bp mRNA linear EST 22-APR-2002  
 DEFINITION INITI1.2-D10.91-A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis cDNA, mRNA sequence.

ACCESSION BQ135036.1 GI:20261135

VERSION EST  
 KEYWORDS Ichthyophthirius multifiliis.  
 SOURCE Ichthyophthirius multifiliis.  
 ORGANISM Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryogenina; Ichthyophthirius.

REFERENCE 1 (bases 1 to 419)  
 Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.  
 An EST database for Ichthyophthirius multifiliis (G5 isolate)  
 Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: [impratt@uga.edu](mailto:impratt@uga.edu)

COMMENT Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.  
 Seq primer: T7  
 High quality sequence start: 306  
 High quality sequence stop: 419  
 PolyA:yes

FEATURES Source  
 /organism="Ichthyophthirius multifiliis"  
 /strain="G5"  
 /db\_xref="taxon:5932"  
 /clone\_lib="G5 trophont cDNA (INIT1)"  
 /note="Vector: pBluescript SK (-) from Lambda Zap II;  
 Site:1: ECORI; Site:2: ECORI; The library was made from trophont PolyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to ECORI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."

BASE COUNT 140 a 74 c 73 g 132 t  
 ORIGIN Query Match 22.2%; Score 294.4; DB 14; Length 419;  
 Best Local Similarity 85.4%; Pred. No. 4.9e-53; Indels 0; Gaps 0;

Matches 328; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 943 AATGGTAATTCGAAAGCTTAAAGTTAATGTTAAAGTGTCCAGTAAGTAAACACT 1002  
 Db 416 AATCGTAATTCGAAAGCTTAAAGTGTCCAGTAAGTAAACACT 357

Qy 1003 CCAGCACATGTCAGGTTAATCTACTTAATGCCACATATGTTGACACATGCT 1062  
 Db 356 TCAGCATCTGTCAGGTTAATGCTACTCAGGCCACATATGTTAATGCT 297

Qy 1063 GCTGGTACAGTACTGATGTCACATCAACTAATTGAGCTTCCGCAACTGAATGT 1122

Db 296 GCTGTACAGTGTGATCATGGTACATCAACTAATTGTCAGTGTAAATGT 237  
 Qy 1123 ACTAAATGCTCTGCTGCTTTCGCACTAAACAAACTGTTTACAGCAGGTACTGAT 1182  
 Db 236 ACTAAATGTTAGGCTAACTGATGTTATGCACTAAACATCGGTTGCGCAGGTACTGAT 177  
 Qy 1183 ACATGTAATGCAATGTTAAATTAATCTCGGTGCAACGCTAAAGTATGCTGAA 1242  
 Db 176 CCATGTAATGCAATGTTAAATTAATCTCCGGTGTCAAGCTRAAGTATAAGCGGAA 117  
 Qy 1243 GCTACTCAAAGTATAATGCGCTCAACTATTCGTAATTTTATGATTCTCTTA 1302  
 Db 116 GCTACTTAAAGCTATAATGCGCAAGTCACATTGCGCAATGTCAGTTCGCAATGGCTTA 57

RESULT 9  
 BQ135189 661 bp mRNA linear EST 22-APR-2002  
 LOCUS BQ135189\_4-D09.91-A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis cDNA, mRNA sequence.

DEFINITION BQ135189  
 VERSION BQ135189.1 GI:20261288  
 KEYWORDS EST  
 SOURCE Ichthyophthirius multifiliis.  
 ORGANISM Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryogenina; Ichthyophthirius.  
 1 (bases 1 to 661)  
 Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.  
 An EST database for Ichthyophthirius multifiliis (G5 isolate)  
 Unpublished (2002)  
 Contact: Cordonnier-Pratt MM  
 REFERENCE Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.  
 TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: [impratt@uga.edu](mailto:impratt@uga.edu)  
 Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.  
 Seq primer: T7  
 High quality sequence start: 306  
 High quality sequence stop: 419  
 PolyA:yes

FEATURES Source  
 /organism="Ichthyophthirius multifiliis"  
 /strain="G5"  
 /db\_xref="taxon:5932"  
 /clone\_lib="G5 trophont cDNA (INIT1)"  
 /note="Vector: pBluescript SK (-) from Lambda Zap II;  
 Site:1: ECORI; Site:2: ECORI; The library was made from trophont PolyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to ECORI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."

BASE COUNT 197 a 127 c 124 g 213 t  
 ORIGIN Query Match 21.2%; Score 280.6; DB 14; Length 661;  
 Best Local Similarity 66.3%; Pred. No. 4.7e-50;  
 Matches 437; Conservative 0; Mismatches 183; Indels 33; Gaps 1;  
 II. Plasmid DNA for sequencing was prepared by mass excision."

Qy 448 GTTTTGGCTGGTGTGGCTGCCGTTACTAGTTAATGTCACCT 507

		FEATURES	source	Location/Qualifiers
Db	1	GATCT <sup>n</sup> GCTTAATACTCCTGAAGTCTCTTAATGTTCTAGGCCATAATGGTTAATGGTAGCTT	60	1. 5'599 /organism="Ichthyophthirius multifiliis" /strain="G5" /db_xref="Taon-5932"
Qy	508	TGCCAACTAAACAAAACGATTCTCCTGCCACTSGAGGCTTAAAGCTTAAAGCTTAAAGCTAACAA	567	2. 5'599 /note="Vector: PBLUEScript SK (-) from Lambda zap II; Site_1: ECoRI; Site_2: BCoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain. Double stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."
Db	61	TGCTAATGAAACAAAGTCGATTCAATAGGCTTAAATGAGCTTAAATGGTAGCTTAAATGGTAGCTAACAA	120	191 a 113 c 111 g 183 t 1 others
Qy	568	TAATGTAACAACTTAATGTCCTACGGCACTGTACTTGAGATGAGCTGACTCTGTTT	627	Query Match Score 19.9%; Length 599; Best Local Similarity 71.6%; Pred. No. 1.7e-46; Matches 346; Conservative 0; Mismatches 137; Indels 0; Gaps 0;
Db	121	TAATGTAACAACTTAATGAGCTTAAATGGTAGCTTAAATGGTAGCTTAAATGGTAGCTAACAA	180	Qy 675 TAATGGCGCTTCTCCCTAAGGTGAAGCTCCGGCTTAAGCTTTGCTGTGGCTGC 734 Db 4.94 TAATGGATAAATTCACCCAGGTTAATTGATGCAATTCCCTGATGCGCTACTGCTGCTTA 435
Qy	628	AATACATAGCCACATTATGTTAAATGGAGACCTTAACTATAATGGGGTTCT	687	Qy 735 CCTCGAGGTGTTGTCGGTTTACTAGTTAATGTTACCTTAAATGCAATAAACAAACGA 794 Db 4.34 AATTCTATGGTTCTCCGGCTTAAATGCTGAGCTTAAATGGTAGCTAGCTGAGTCATAACCAA 375
Db	181	ACTTAAATCAATCTCATAAATGACTCTTTAAATGACTCTTTAAATGGTAGCTTAAATGGGCAAT	240	Qy 795 TTCTCTGGCCACTGAGCTGGCTTAAGCTTAATGGCACATAATGGCTACTTAAATGTCC 854 Db 374 TTCTTAATCCAGATCAGGTCTGTAGCTTAATGGCGACTGAATGTTGGCTAATGGTCC 315
Qy	688	CCTTAAGGTGAAGCPCCTCGCTTAA-----714		Qy 855 AACATGCGACTGCAATTCAGAGGGAGTGACATTGTTTTAGTAACTTCACATAATG 914 Db 314 TGCTGGGACTCTGTTGAGCGGACTAACCTACTTAACTGTCACTCTCATATAATG 255
Db	241	CCTTCAGCTAGAAATCCTGGTAATGGTAACTTCACTCCAGGTAAATTGTAATGGTAGCTTAAATCCT	300	Qy 915 TTCTTAATGGCATTTGCTTAATCTTAAATGTTAATGGTAAATTGAGGTTAAAGTTAATG 974 Db 254 TTCTTAATGGTAAAGCTGGCTTTACTAAATAGTAAATGGCTAATGGTCAATGGTCC 195
Qy	715	GTTTTGCTGCTGCTGGCTGGCTGGCAGGTGTTCTGCCACTTGAGCTTAATGTTAATGTT	774	Qy 975 TTAAAGTGTCGAGTAAACACTGCAATGGTAAACTTGCAACTGTTAATGGTAGCTTAAATGGTAGCTTA 1034 Db 194 CAATATGTTGCGTAGTAAACTGTTGAGCTTAAACTGTTGAGCTTAAATGGTAGCTTAAATGGTAGCTTC 135
Db	301	GATGCTGCTACTGTGCTTAAATTCCTATGGTCTGGCTTAAATGGTAGCTTAAATGGTAGCTAACAA	360	Qy 1035 AGCCACATAATGTTGACCCACATGTCCTGCTGTTACAGTACTGATGATGGAAACATCAAC 1094 Db 134 AGCCACATAATGTTAAACGATTGCTGCTGTTACAGGGTTGATCATCAC 75
Qy	775	TGCCAAATAACAAAACGATTCTCCTGCCACTTGAGCTTAATGGTAGCTTAAATGGTAGCTAACAA	834	Qy 1095 TAATTTGTAGCTTCCGGCAACTGTAATGTTAATGGTAAATTGAGGTTAAAGTTAATG 1154 Db 74 TAATTTGTAGCTTCCGGCAACTGTAATGTTAATGGTAAATTGAGGTTAAAGTTAATG 15
Db	361	TGCGATTCAAAAGAACCAATTCTTAATCAGATCAGCTTCTGGCTTAATGGGCA 420		Qy 1155 AAC 1157 Db 14 AAC 12
Qy	835	TAATGGCAGTACTTAAATGTCCTAACTGGACTGCAATTGCAACTTGTGTTT	894	RESULT 10
Db	421	TAATGTCGACTGAATGTCCTGCTGGACTCTGTTGAGCTAACCTACTTA	480	LOCUS BQ134821_c
Qy	895	AGTAAATTCAATCCAAATGTTCTTAATGCAATTGCTTAATTAATGTTAATGTTAATTTC	954	DEFINITION INIT1_4-D09_b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis mRNA sequence.
Db	481	ACTGTTATCCTCCTCATAAATGTTGTTAAATGTTGCAACTTAAATGTTAATTTC	540	ACCESSION BQ134821
Qy	955	GAAGCAGGTAAAAGTAAATGTTAAAGTGTCCAGTAAGTAAACTACTCAGCACATGT	1014	VERSION BQ134821.1
Db	541	GAACAGGTAAAAGTAAATGTTAAATGCAATTGTTGCAACTAAGTGTCAAGTCTGGATCTGT	600	KEYWORDS EST.
Qy	1015	CCAGGTAATAATGCTACTTAAGCCACATAATGTTGACCAACATGTCGTTGTTAGT	1073	SOURCE Ichthyophthirius multifiliis.
Db	601	CCAGGTAATAATGCTACTTCATAAATGTTGTTAAATGTTGACCAACATGTCGTTGTTAGT	659	ORGANISM Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenida; Ichthyophthirius.
REFERENCE		TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)		RESULT 11
JOURNAL		COMMENT Unpublished (2002)		LOCUS BQ134985
COMMENT		Contact: Cordonnier-Pratt, M.M., Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-3721, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: <a href="mailto:umpat@uga.edu">umpat@uga.edu</a>		DEFINITION INIT1_2_G01_b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis mRNA sequence.
AUTHORS		Sequences have been trimmed to exclude PolyA, vector, and regions below phred quality 16. The threshold for highest quality sequence is 20.		ACCESSION BQ134985
TITLE		Seq primer: JEN REV High quality sequence stop: 506 POLYA-No:		KEYWORDS EST.
				ORGANISM Ichthyophthirius multifiliis
				REFERENCE 1 (bases 1 to 592)
				AUTHORS Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A., Dickerson, H., Lin, T.-L., and Pratt, L.H.
				TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)

JOURNAL		PUBLISHED (2002)		CONTACT: Cordonnier-Pratt MM		LABORATORY FOR GENOMICS AND BIOINFORMATICS		THE UNIVERSITY OF GEORGIA, DEPARTMENT OF PLANT BIOLOGY		PLANT SCIENCES BUILDING, RM. 2502, ATHENS, GA 30602-7271, USA		TEL: 706 542 1860		FAX: 706 583 0210		EMAIL: <a href="mailto:impratt@uga.edu">impratt@uga.edu</a>		SEQUENCES HAVE BEEN TRIMMED TO EXCLUDE POLYA, VECTOR, AND REGIONS BELOW PHRED QUALITY 16. THE THRESHOLD FOR HIGHEST QUALITY SEQUENCE IS 20.		SEQ. PRIMER: JEN REV		HIGH QUALITY SEQUENCE STOP: 575		POLYA-NO.		LOCATION/QUALIFIERS		ORGANISM		ICHTHYOPHTHIRIUS MULTIFILIIS		EUKARYOTA; ALVEOLATA; CILIOPHORA; OLIGOHYMENOPHOREA; HYMENOSTOMATIDA; OPHRYGLENINA; ICHTHYOPHTHIRIUS.		RESULT 12		BO134810		538 BP		mRNA LINEAR		EST 22-APR-2002	
FEATURES		SOURCE		LOCUS		DEFINITION		INIT1_1-C08_b1-A006 G5		TROPHON CDNA (INIT1) ICHTHYOPHTHIRIUS		INIT1_1-C08_b1-A006 G5		mRNA		mRNA		mRNA		mRNA		mRNA		mRNA		mRNA		mRNA															
ACCESSION		VERSION		REFERENCE		1 (bases 1 to 538)		1		Hymenostomatida; Ophryglenina; Ichthyophthirius.		EST		EST		EST		EST		EST		EST		EST		EST																	
VERSION		AUTHORS		CLARK, T., CORDONNIER-PRATT, M.-M., SUDMAN, M., WENTZEL, V., GINGLE, A., DICKERSON, H., LIN, T.-L., AND PRATT, L.H.		KEYWORDS		ICHTHYOPHTHIRIUS MULTIFILIIS		An EST database for Ichthyophthirius multifiliis (G5 isolate)		UNPUBLISHED (2002)		CONTACT: CORDONNIER-PRATT, MM		HUMANOMONADIDA; OPHRYGLENINA; ICHTHYOPHTHIRIUS.		UNPUBLISHED		UNPUBLISHED		UNPUBLISHED		UNPUBLISHED		UNPUBLISHED		UNPUBLISHED															
KEYWORDS		TITLE		COMMENT		JOURNAL		COMMENT		JOURNAL		COMMENT		JOURNAL		COMMENT		JOURNAL		COMMENT		JOURNAL		COMMENT		JOURNAL																	
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Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass

## COMMENT

Qy	675	TAATGGGTTCTCTTAAGGTGAAGCTCCGGCTTTAAGTTTTGCTGGTGTGCG 734
Db	599	TAATGGCAATCCCTACCTCAAAATCCGGTATGGATAATTCACTCAGGTAAATT 658
Qy	735	CGCTCAGGTGTCGGTTACT 759
Db	659	GATTGCAAATCCGTGCGCTACT 683

Search completed: February 16, 2003, 22:24:44  
Job time : 1372.09 secs

